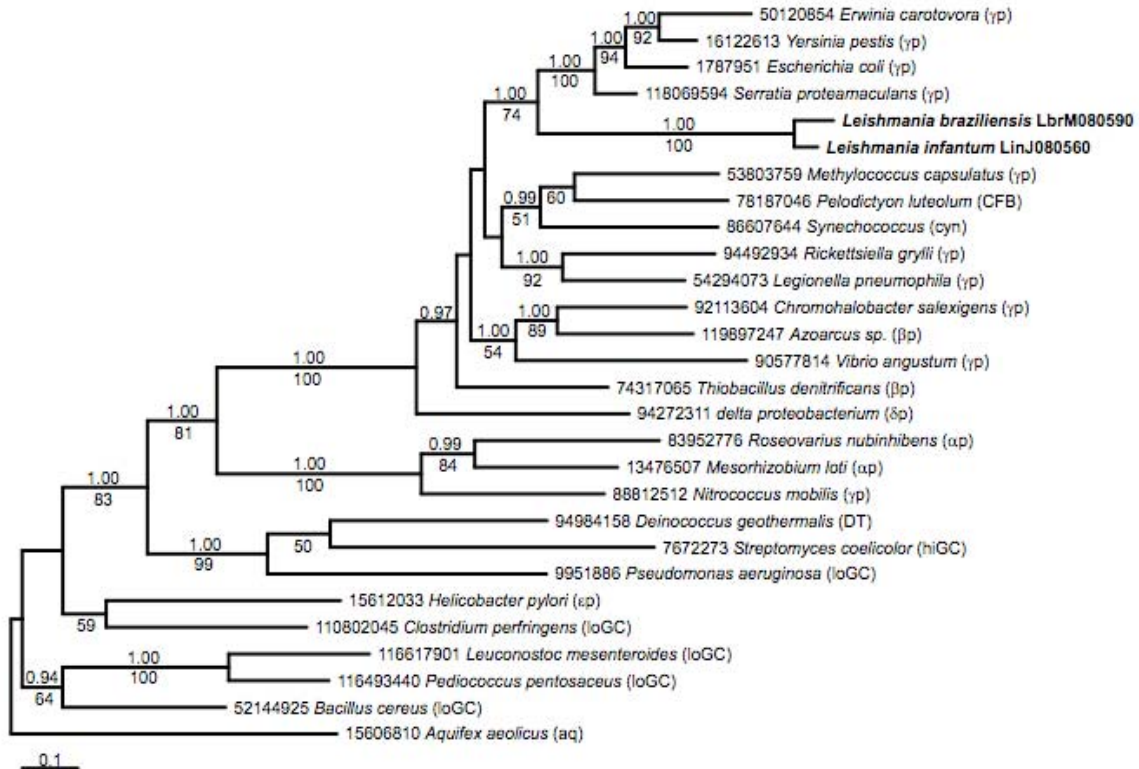


Supplementary Fig S3. The Phylogenetic tree for cyclopropane fatty acyl phosholipid synthase (CFAS).



The CFAS gene in *L. infantum* and *L. braziliensis*. The closest orthologues in the public databases to this gene are all prokaryotic suggesting that this gene has a bacterial origin and may have been acquired by lateral gene transfer. The tree shown was derived by Bayesian inference and further tested by maximum likelihood bootstrapping. Posterior probabilities above 0.90 and bootstrap support values over 50% are indicated above and below the lines, respectively. Branches are drawn to scale as indicated by the scale bar at the lower left (mutations per site). Higher level classifications of bacteria are indicated in brackets following their names for actinobacteria (hiGC), firmicutes (loGC), cyanobacteria (cyn), deinococci (DT), hydrogenobacteria (aq), chlorobi-bacteroids (CFB), and alpha-, beta-, delta, epsilon and gamma-proteobacteria.